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SYSTEM:OS - DIALOG OneSearch
File 155:MEDLINE(R) 1966-2003/Mar W1
(c) format only 2003 The Dialog Corp.
File 50:CAB Abstracts 1972-2003/Jan
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See Help News50 for details.
File 357:Derwent Biotech Res. _1982-2003/Mar W2
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Set Items Description
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Set Items Description
S1 12032 PARVO?
S2 71090 MVM OR RODENT OR LUIII OR LU111 OR H1 OR H(W)1
S3 457 S1 AND S2
S4 208 REPLICAT? AND S3
S5 34 (ORIGIN OR ORIGINS) AND S4
S6 32 RD (unique items)
S7 22 S6 AND (LEFT OR RIGHT OR 3 OR 5 OR 3' OR 5')
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S9 30 RD (unique items)

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7/7/8 (Item 8 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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08223506 94357188 PMID: 8076610
An asymmetric nucleotide in the parvoviral 3' hairpin directs segregation of a single active origin of DNA replication.
Cotmore S F; Tattersall P

Department of Laboratory Medicine, Yale University School of Medicine, New Haven, CT 06510.
EMBO journal (ENGLAND) Sep 1 1994, 13 (17) p4145-52, ISSN 0261-4189 Journal Code: 8208664
Contract/Grant No.: AI26109; AI; NIAID; CA29303; CA; NCI
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
The 3' telomere of the linear single-stranded DNA genome of minute virus of mice (MVM), a murine parvovirus, can assume a complex hairpin structure. This contains a stem in which there is a mismatched 'bubble' sequence where a GA doublet opposes a GAA triplet. During replication, this hairpin is copied to form an imperfect palindrome which bridges adjacent genomes in a dimer duplex intermediate, leaving the two 'bubble' sequences embedded in potential replication origins on either side of the axis of symmetry. Such junctions are resolved asymmetrically in vitro in a DNA synthetic reaction which requires the viral initiator protein NS1. We show that the sequence surrounding the doublet is a potent origin, but the analogous region containing the triplet is completely inactive. The active origin is approximately 50 bp long, extending from an Activated Transcription Factor binding site at one end to a position some 7 bp beyond the major initiation site, to which NS1 ultimately becomes covalently attached. The actual sequence of the GA doublet is unimportant, but insertion of any third nucleotide here inactivates the origin, indicating that it represents a critical spacer element. Segregation of this asymmetry, therefore, allows the virus to confine replication initiation to one particular telomeric configuration.
Record Date Created: 19941005

7/7/9 (Item 9 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.
08026401 94149826 PMID: 8107203
Use of an autonomous parvovirus vector for selective transfer of a foreign gene into transformed human cells of different tissue origins and its expression therein.
Dupont F; Tenenbaum L; Guo L P; Spegelaere P; Zeicher M; Rommelaere J
Department of Molecular Biology, Universite Libre de Bruxelles, Rhode Saint Genese, Belgium.
Journal of virology (UNITED STATES) Mar 1994, 68 (3) p1397-406, ISSN 0022-538X Journal Code: 0113724
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
In this work, we report the transduction of a chloramphenicol acetyltransferase (CAT) reporter gene into a variety of normal and transformed human cells of various tissue origins. The vector used was MVM/P38cat, a recombinant of the prototype strain of the autonomous parvovirus minute virus of mice (MVMp). The CAT gene was inserted into the capsid-encoding region of the infectious molecular clone of MVMp genome, under the control of the MVM P38 promoter. When used to transfect permissive cells, the MVM/P38cat DNA was efficiently replicated and expressed the foreign CAT gene at high levels. By cotransfecting with a helper plasmid expressing the capsid proteins, it was possible to produce mixed virus stocks containing MVM/P38cat infectious particles and variable amounts of recombinant MVM. MVM/P38cat viral particles were successfully used to transfer the CAT gene and to express it in a variety of human cells. Both viral DNA replication and P38-driven CAT expression were achieved in fibroblasts, epithelial cells, T lymphocytes, and macrophages in a transformation-dependent way, but with an efficiency depending on the cell type. In transformed B lymphocytes, however, the vector was not replicated, nor did it express the CAT gene.
Record Date Created: 19940323

7/7/13 (Item 13 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.
03968667 82242308 PMID: 6284985
DNA sequence of the 5' terminus containing the replication origin of parvovirus replicative form DNA.
Rhode S L; Klaassen B
Journal of virology (UNITED STATES) Mar 1982, 41 (3) p990-9, ISSN 0022-538X Journal Code: 0113724
Contract/Grant No.: CA-25866; CA; NCI; CA26801; CA; NCI
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
The nucleotide sequence of the 5' terminus of the parvovirus H-1 was determined. There are two orientations of the 242-base-pair terminal palindrome in native replicative form DNA, one inverted with respect to the other. Adjacent to the terminal palindrome is an AT-rich region that is noncoding and contains a 55-base-pair tandem repeat. The addition mutant of H-1, DI-1, was also sequenced in this region and shown to have three copies of the tandem repeat sequence. Similarly, the related parvovirus H-3 contains only one copy of this repeat sequence. This region contains the replication origin for parvovirus replicative form DNA replication. Some of the implications of these results are discussed.
Record Date Created: 19820910

7/7/14 (Item 14 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

(c) format only 2003 The Dialog Corp. All rts. reserv.
03186483 80001961 PMID: 225040
Structure of the 3' hairpin termini of four rodent parvovirus genomes: nucleotide sequence homology at origins of DNA replication.
Astell C R; Smith M; Chow M B; Ward D C
Cell (UNITED STATES) Jul 1979, 17 (3) p691-703, ISSN 0092-8674 Journal Code: 0413066
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
The nucleotide sequences of the 3' termini of the DNA from four autonomous rodent parvoviruses have been determined. The terminus of each genome exists as a Y-shaped hairpin structure involving 115 or 116 nucleotides. The sequence of this region of DNA is highly conserved and shows no evidence of internal sequence heterogeneity, a characteristic which is observed in the terminal nucleotide sequence of the helper-dependent, adeno-associated viruses (Berns et al., 1978a). The implications of these results with respect to the models of parvovirus DNA replication are discussed.
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** New CURRENT Year ranges installed **

SYSTEM:OS - DIALOG OneSearch
File 155:MEDLINE(R) 1966-2003/Mar W1
(c) format only 2003 The Dialog Corp.
File 50:CAB Abstracts 1972-2003/Jan
(c) 2003 CAB International
*File 50: Truncating CC codes is recommended for full retrieval.
See Help News50 for details.
File 357:Derwent Biotech Res. _1982-2003/Mar W2
(c) 2003 Thomson Derwent & ISI
*File 357: File is now current. See HELP NEWS 357.
Alert feature enhanced for multiple files, etc. See HELP ALERT.

Set Items Description
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9/7/1 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.
11292356 21329483 PMID: 11435581
Minute virus of mice initiator protein NS1 and a host KDWK family transcription factor must form a precise ternary complex with origin DNA for nicking to occur.
Christensen J; Cotmore S F; Tattersall P
Institute of Medical Microbiology and Immunology, University of Copenhagen, Panum Institute, Copenhagen 2200 N, Denmark.
Journal of virology (United States) Aug 2001, 75 (15) p7009-17, ISSN 0022-538X Journal Code: 0113724
Contract/Grant No.: AI26109; AI; NIAID
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Parvoviral rolling hairpin replication generates palindromic genomic concatemers whose junctions are resolved to give unit-length genomes by a process involving DNA replication initiated at origins derived from each viral telomere. The left-end origin of minute virus of mice (MVM), oriL, contains binding sites for the viral initiator nickase, NS1, and parvovirus initiation factor (PIF), a member of the emerging KDWK family of transcription factors. oriL is generated as an active form, oriL(TC), and as an inactive form, oriL(GAA), which contains a single additional nucleotide inserted between the NS1 and PIF sites. Here we examined the interactions on oriL(TC) which lead to activation of NS1 by PIF. The two subunits of PIF, p79 and p96, cooperatively bind two ACGT half-sites, which can be flexibly spaced. When coexpressed from recombinant baculoviruses, the PIF subunits preferentially form heterodimers which, in the presence of ATP, show cooperative binding with NS1 on oriL, but this interaction is preferentially enhanced on oriL(TC) compared to oriL(GAA). Without ATP, NS1 is unable to bind stably to its cognate site, but PIF facilitates this interaction, rendering the NS1 binding site, but not the nick site,

resistant to DNase I. Varying the spacing of the PIF half-sites shows that the distance between the NS1 binding site and the NS1-proximal half-site is critical for nickase activation, whereas the position of the distal half-site is unimportant. When expressed separately, both PIF subunits form homodimers that bind site specifically to oriL, but only complexes containing p79 activate the NS1 nickase function.
Record Date Created: 20010703

9/7/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.
10570550 20094920 PMID: 10627544
Two widely spaced initiator binding sites create an HMG1-dependent parvovirus rolling-hairpin replication origin.
Cotmore S F; Christensen J; Tattersall P
Departments of Laboratory Medicine, Yale University School of Medicine, New Haven, Connecticut 06510, USA.
Journal of virology (UNITED STATES) Feb 2000, 74 (3) p1332-41, ISSN 0022-538X Journal Code: 0113724
Contract/Grant No.: AI26109; AI; NIAID; CA29303; CA; NCI
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Minute virus of mice (MVM) replicates via a linearized form of rolling-circle replication in which the viral nickase, NS1, initiates DNA synthesis by introducing a site-specific nick into either of two distinct origin sequences. In vitro nicking and replication assays with substrates that had deletions or mutations were used to explore the sequences and structural elements essential for activity of one of these origins, located in the right-end (5') viral telomere. This structure contains 248 nucleotides, most-favorably arranged as a simple hairpin with six unpaired bases. However, a pair of opposing NS1 binding sites, located near its outboard end, create a 33-bp palindrome that could potentially assume an alternate cruciform configuration and hence directly bind HMG1, the essential cofactor for this origin. The palindromic nature of this sequence, and thus its ability to fold into a cruciform, was dispensable for origin function, as was the NS1 binding site occupying the inboard arm of the palindrome. In contrast, the NS1 site in the outboard arm was essential for initiation, even though positioned 120 bp from the nick site. The specific sequence of the nick site and an additional NS1 binding site which directly orients NS1 over the initiation site were also essential and delimited the inboard border of the minimal right-end origin. DNase I and hydroxyl radical footprints defined sequences protected by NS1 and suggest that HMG1 allows the NS1 molecules positioned at each end of the origin to interact, creating a distortion characteristic of a double helical loop.
Record Date Created: 20000207

9/7/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.
10009020 98440503 PMID: 9765384
High-mobility group 1/2 proteins are essential for initiating rolling-circle-type DNA replication at a parvovirus hairpin origin.
Cotmore S F; Tattersall P
Departments of Laboratory Medicine, Yale University School of Medicine, New Haven, Connecticut 06510, USA.
Journal of virology (UNITED STATES) Nov 1998, 72 (11) p8477-84, ISSN 0022-538X Journal Code: 0113724
Contract/Grant No.: AI26109; AI; NIAID; CA29303; CA; NCI
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Rolling-circle replication is initiated by a replicon-encoded endonuclease which introduces a single-strand nick into specific origin sequences, becoming covalently attached to the 5' end of the DNA at the nick and providing a 3' hydroxyl to prime unidirectional, leading-strand synthesis. Parvoviruses, such as minute virus of mice (MVM), have adapted this mechanism to amplify their linear single-stranded genomes by using hairpin telomeres which sequentially unfold and refold to shuttle the replication fork back and forth along the genome, creating a continuous, multimeric DNA strand. The viral initiator protein, NS1, then excises individual genomes from this continuum by nicking and reinitiating synthesis at specific origins present within the hairpin sequences. Using in vitro assays to study ATP-dependent initiation within the right-hand (5') MVM hairpin, we have characterized a HeLa cell factor which is absolutely required to allow NS1 to nick this origin. Unlike parvovirus initiation factor (PIF), the cellular complex which activates NS1 endonuclease activity at the left-hand (3') viral origin, the host factor which activates the right-hand hairpin elutes from phosphocellulose in high salt, has a molecular mass of around 25 kDa, and appears to bind preferentially to structured DNA, suggesting that it might be a member of the high-mobility group 1/2 (HMG1/2) protein family. This prediction was confirmed by showing that purified calf thymus HMG1 and recombinant human HMG1 or murine HMG2 could each substitute for the HeLa factor, activating the NS1 endonuclease in an origin-specific nicking reaction.
Record Date Created: 19981105

9/7/7 (Item 7 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.
09268859 97151130 PMID: 8995666
A novel cellular site-specific DNA-binding protein cooperates with the viral NS1 polypeptide to initiate parvovirus DNA replication.

Christensen J; Cotmore S F; Tattersall P
Department of Laboratory Medicine, Yale University School of Medicine, New Haven, Connecticut 06510, USA.
Journal of virology (UNITED STATES) Feb 1997, 71 (2) p1405-16, ISSN 0022-538X Journal Code: 0113724
Contract/Grant No.: AI26109; AI; NIAID
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Replication of linear single-stranded parvovirus DNA proceeds by a rolling-hairpin mechanism which generates long, palindromic, duplex concatamers. Processing to monomer length requires initiation from origins of DNA replication located at the 3' and 5' ends of each embedded monomer, reactions which can be recapitulated in vitro for minute virus of mice (MVM). To determine which cellular proteins were essential for replication from these origins, S100 extracts from 293S cells were fractionated on phosphocellulose. When recombined, these fractions were able to support replication in vitro, dependent on the viral initiator protein NS1, using plasmid forms of the 5' origin or the minimal 3' origin as templates. Fraction P-cell 1 contains two factors, replication protein A (RPA) and proliferating-cell nuclear antigen (PCNA), known to be essential for simian virus 40 replication in vitro. When P-cell 1 was replaced with purified recombinant RPA and PCNA, NS1-mediated MVM replication initiated from the 5' origin but not from the 3' origin. The 3' origin is a 50-bp sequence containing three distinct recognition elements, an NS1 binding site, a site at which NS1 nicks the DNA to generate the priming 3' OH, and a region containing a consensus activated transcription factor (ATF) binding site. To identify the missing factor(s) for 3' origin replication, P-cell 1 was fractionated by further chromatography and active fractions were identified by their ability to complement RPA, PCNA, and P-cell 2 for NS1-mediated, origin-specific replication. Gel shift and UV cross-linking analysis of the replication-competent fractions revealed a novel 110-kDa sequence-specific DNA binding protein which recognized the consensus ATF binding site region of the origin and which we have termed parvovirus initiation factor, or PIF. Binding of PIF appears to activate the endonuclease function of NS1, allowing efficient and specific nicking of the 3' minimal origin under stringent conditions in vitro.
Record Date Created: 19970218

9/7/8 (Item 8 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08839799 96201434 PMID: 8609486
Molecular characterization of newly recognized rodent parvoviruses.
Besselsen D G; Pintel D J; Purdy G A; Besch-Williford C L; Franklin C L; Hook R R; Riley L K
Department of Veterinary Pathology, University of Missouri, Columbia 65211, USA.
Journal of general virology (ENGLAND) May 1996, 77 (Pt 5) p899-911, ISSN 0022-1317 Journal Code: 0077340
Contract/Grant No.: DHHS5 P01 RR08624; RR; NCRR; DHHS5 T32 RR07004; RR; NCRR
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Several autonomous rodent parvoviruses distinct from the prototypic rodent parvoviruses have been isolated. These include variants of a mouse parvovirus (MPV), a hamster isolate designated hamster parvovirus (HaPV), and a variant strain of minute virus of mice (MVM) designated MVM-Cutter or MVM(c). In this study, the DNA sequence of the coding regions of the viral genome and the predicted protein sequences for each of these new isolates were determined and compared to the immunosuppressive and prototypic strains of MVM [MVM(i) and MVM(p)], the rodent parvovirus H-1, and LuIII, an autonomous parvovirus of uncertain host origin. Sequence comparisons showed that the MPV isolates were almost identical, HaPV was very similar to MPV, and MVM(c) was most similar to MVM(i) and MVM(p). Haemagglutination inhibition assays revealed that MPV and HaPV represent two serotypes distinct from previously characterized rodent parvovirus serotypes while MVM(c) belongs to the MVM serotype. Each of the newly isolated rodent parvoviruses was shown to encapsidate a predominantly negative-sense 5 kb DNA genome and to encode two nonstructural proteins (NS1 and NS2) and two structural viral proteins (VP1 and VP2). These studies indicate that MPV and HaPV are autonomous parvoviruses distinct from previously characterized parvoviruses and MVM(c) is a variant strain of MVM distinct from MVM(i) and MVM(p).
Record Date Created: 19960530

9/7/9 (Item 9 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08509313 95266299 PMID: 7747462
Sequence motifs in the replicator protein of parvovirus MVM essential for nicking and covalent attachment to the viral origin: identification of the linking tyrosine.
Nuesch J P; Cotmore S F; Tattersall P
Department of Laboratory Medicine, Yale University School of Medicine, New Haven, Connecticut 06510, USA.
Virology (UNITED STATES) May 10 1995, 209 (1) p122-35, ISSN 0042-6822 Journal Code: 0110674
Contract/Grant No.: AI26109; AI; NIAID
Document type: Journal Article
Languages: ENGLISH

Main Citation Owner: NLM
Record type: Completed
Parvoviral DNA replication has many features in common with prokaryotic rolling circle replication (RCR), including the pivotal role of an initiator protein which introduces a site-specific, single strand nick into a duplex origin sequence. In this process, the protein becomes covalently attached to the new 5' end of the DNA, while making available a 3' hydroxyl to prime de novo synthesis. Sequence comparisons of prokaryotic RCR initiators has revealed a set of three common motifs, two of which, a putative metal coordination site and a downstream active-site tyrosine motif, could be tentatively identified in parvoviral replicator proteins. We have introduced mutations into the NS1 gene of the murine parvovirus minute virus of mice (MVM), in the putative metal coordination site at H129, and into the three candidate tyrosine motifs at Y188, Y197, and Y210. Histidine-tagged mutant proteins were expressed in HeLa cells from recombinant vaccinia virus vectors and partially purified. None of the mutant proteins were able to initiate replication of origin-containing plasmids in vitro, and each showed impaired site-specific binding to the viral origin, with Y188 and Y197 being most severely defective. If this deficiency was minimized using low salt conditions, however, Y188 and Y197 mutant proteins were able to nick and become covalently attached to origin DNA, whereas Y210 and H129 mutant proteins were not, suggesting that the latter residues are part of the catalytic site of the NS1 nickase. Transfer of [32P]phosphate from substrate DNA to NS1, followed by cyanogen bromide cleavage of the complex, gave the single, labeled peptide consistent with Y210 being the linking tyrosine.
Record Date Created: 19950612

9/7/11 (Item 11 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08026401 94149826 PMID: 8107203
Use of an autonomous parvovirus vector for selective transfer of a foreign gene into transformed human cells of different tissue origins and its expression therein.
Dupont F; Tenenbaum L; Guo L P; Spegelaere P; Zeicher M; Rommelaere J
Department of Molecular Biology, Universite Libre de Bruxelles, Rhode Saint Genese, Belgium.
Journal of virology (UNITED STATES) Mar 1994, 68 (3) p1397-406, ISSN 0022-538X Journal Code: 0113724
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
In this work, we report the transduction of a chloramphenicol acetyltransferase (CAT) reporter gene into a variety of normal and transformed human cells of various tissue origins. The vector used was MVM/P38cat, a recombinant of the prototype strain of the autonomous parvovirus minute virus of mice (MVMp). The CAT gene was inserted into the capsid-encoding region of the infectious molecular clone of MVMp genome, under the control of the MVM P38 promoter. When used to transfect permissive cells, the MVM/P38cat DNA was efficiently replicated and expressed the foreign CAT gene at high levels. By cotransfecting with a helper plasmid expressing the capsid proteins, it was possible to produce mixed virus stocks containing MVM/P38cat infectious particles and variable amounts of recombinant MVM. MVM/P38cat viral particles were successfully used to transfer the CAT gene and to express it in a variety of human cells. Both viral DNA replication and P38-driven CAT expression were achieved in fibroblasts, epithelial cells, T lymphocytes, and macrophages in a transformation-dependent way, but with an efficiency depending on the cell type. In transformed B lymphocytes, however, the vector was not replicated, nor did it express the CAT gene.
Record Date Created: 19940323

9/7/16 (Item 16 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06162382 89243219 PMID: 2541561
Sequence organization in regulatory regions of DNA of minute virus of mice.
Bodnar J W
Northeastern University, Department of Biology, Boston, MA 02115.
Virus genes (UNITED STATES) Mar 1989, 2 (2) p167-82, ISSN 0920-8569 Journal Code: 8803967
Contract/Grant No.: GM-35238; GM; NIGMS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Analysis of the nucleotide sequence of minute virus of mice (MVM) DNA indicates that the DNA termini contain clusters of potential DNA regulatory elements and that there are repetitive DNA elements highly reiterated throughout the entire genome, which may also have a role in DNA function. The left end of MVM DNA, which contains the promoter for the nonstructural genes, has a cluster of DNA elements that includes homologies to the polyoma virus enhancer, three copies of an E1A-inducible transcription factor (ATF) binding site, and a potential Z-DNA element. The MVM right end, which contains the origin of DNA replication, has a cluster of DNA elements that includes several homologies to the polyoma virus replication origin and a potential Z-DNA element. In addition, oligonucleotide frequency analysis indicates the presence of highly recurring sequence elements throughout the entire MVM genome that may be involved in regulation. This computer-aided analysis suggests similarities and significant differences in regulatory sequence organization between MVM and

polyoma virus, and identifies specific DNA elements for future genetic characterization.
Record Date Created: 19890622

9/7/17 (Item 17 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05031604 86094220 PMID: 3866226
Proteins tightly associated with the termini of replicative form DNA of Kilham rat virus, an autonomous parvovirus.
Wobbe C R; Mitra S
Proceedings of the National Academy of Sciences of the United States of America (UNITED STATES) Dec 1985, 82 (24) p8335-9, ISSN 0027-8424 Journal Code: 7505876
Contract/Grant No.: GM7438; GM; NIGMS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Revie et al. [Revie, D., Tseng, B. Y., Grafstrom, R. H. & Goulian, M. (1979) Proc. Natl. Acad. Sci. USA 76, 5539-5543] have proposed that the double-stranded replicative form (RF) DNA of the autonomous rodent parvovirus H-1 has protein of 60 kDa covalently bound at its 5' termini. We present evidence that the RF DNA of a similar rodent parvovirus, Kilham rat virus (KRV), also has covalently bound protein. NaDodSO4/polyacrylamide gel electrophoresis of purified, 125I-labeled RF DNA shows that proteins of 68-72, 66, 64, and 55 kDa copurify with the DNA during velocity and equilibrium sedimentation in the presence of detergents and 4 M guanidine HCl. Phenol extraction in the presence of 2-mercaptoethanol removes the 68- to 72-kDa proteins, but the 66-, 64-, and 55-kDa proteins remain tightly, but noncovalently, bound. The latter polypeptides also appear to associate with protease-treated RF DNA when mixed with uninfected cell extract. Following removal of these proteins by electrophoresis in NaDodSO4/agarose gels, two proteins (called RF TP-90 and RF TP-40), of about 90 and 40 kDa, become evident. These remain bound to the DNA and are released only after nuclease digestion of the DNA. These two proteins, apparently not of viral origin, are associated with terminal restriction fragments of the RF DNA and appear to be covalently bound to the 5' termini of both strands.
Record Date Created: 19860207

9/7/19 (Item 19 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

03968667 82242308 PMID: 6284985
DNA sequence of the 5' terminus containing the replication origin of parvovirus replicative form DNA.
Rhode S L; Klaassen B
Journal of virology (UNITED STATES) Mar 1982, 41 (3) p990-9, ISSN 0022-538X Journal Code: 0113724
Contract/Grant No.: CA-25866; CA; NCI; CA26801; CA; NCI
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
The nucleotide sequence of the 5' terminus of the parvovirus H-1 was determined. There are two orientations of the 242-base-pair terminal palindrome in native replicative form DNA, one inverted with respect to the other. Adjacent to the terminal palindrome is an AT-rich region that is noncoding and contains a 55-base-pair tandem repeat. The addition mutant of H-1, DI-1, was also sequenced in this region and shown to have three copies of the tandem repeat sequence. Similarly, the related parvovirus H-3 contains only one copy of this repeat sequence. This region contains the replication origin for parvovirus replicative form DNA replication. Some of the implications of these results are discussed.
Record Date Created: 19820910

9/7/24 (Item 24 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

02530459 77097298 PMID: 851476
Replication process of the parvovirus H-1. VI. Characterization of a replication terminus of H-1 replicative-form DNA.
Rhode S L
Journal of virology (UNITED STATES) Feb 1977, 21 (2) p694-712, ISSN 0022-538X Journal Code: 0113724
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
The linear duplex replicative form (RF) DNA of the parvovirus H-1 has been characterized with respect to cleavage by the bacterial restriction endonuclease of Escherichia coli, EcoRI. RF DNA has a single cleavage site 0.22 genome length from the left end of the molecule. The molecular weight of H-1 RF DNA determined by gel electrophoresis is 3.26 X 10(6). H-1 RF DNA has been found to dimerize by hydrogen-bounded linkage at the molecular left end, and in some molecules the viral strand is covalently linked to the complementary strand. Some 10% of monomeric RF DNA also has a covalent linkage between the viral and complementary strands at the left end. The EcoRI-B fragment, containing the left end of the RF molecule, appears to be a replication terminus by its labeling characteristics for both RF and progeny DNA synthesis. These findings suggest that the left end of H-1 RF DNA has some type of "turn-around" structure and that this end is not an origin for DNA synthesis.
Record Date Created: 19770331

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? log hold
    06mar03 10:14:28 User208669 Session D2225.3
       $2.33   0.729 DialUnits File155
         $0.00  25 Type(s) in Format  6
         $2.31  11 Type(s) in Format  7
       $2.31  36 Types
   $4.64  Estimated cost File155
       $0.65   0.144 DialUnits File50
         $0.00  1 Type(s) in Format  6
       $0.00  1 Types
   $0.65  Estimated cost File50
       $2.50   0.139 DialUnits File357
         $0.00  4 Type(s) in Format  6
       $0.00  4 Types
   $2.50  Estimated cost File357
       OneSearch, 3 files,  1.012 DialUnits FileOS
   $2.80  TELNET
  $10.59  Estimated cost this search
  $10.59  Estimated total session cost   1.012 DialUnits
Logoff: level 02.12.60 D  10:14:28
```